

**Amendments to the Specification:**

Please insert the following new paragraph as the first paragraph after the title on page 1:

**--CROSS-REFERENCES TO RELATED APPLICATIONS**

This application is a divisional of U.S. Application No. 09/428,156, filed October 27, 1999, which is incorporated herein by reference in its entirety for all purposes.--

Please replace the paragraph beginning on page 5, line 18 with the following rewritten paragraph:

--Figure 1 shows a cDNA sequence (SEQ ID NO: 1) for human KSP, GenBank accession number X85137, wherein the start and stop codons are shown underlined and in bold, beginning at positions 11 and 3182, respectively.--

Please replace the paragraph beginning one page 5, line 21 with the following rewritten paragraphs:

--Figure 2 shows an amino acid sequence ~~encoding~~ for human KSP (SEQ ID NO: 2).--

Please replace the paragraph beginning on page 5, line 22 with the following rewritten paragraph:

--Figure 3 shows a nucleic acid sequence encoding a fragment of KSP, termed ~~KSPL360~~ KSP-L360 herein (nucleotides 1 to 1080 of SEQ ID NO:3). KSP-L360 plus the nucleotides encoding a C-terminal myc epitope and 6-histidine tag collectively include the nucleotides of SEQ ID NO:3. Portions differing from the sequences of Figures 1 and 2 are indicated in bold typeface and are underlined. ~~Residues at the C-terminus include a myc epitope and a 6-histidine tag.~~--

Please replace the paragraph beginning on page 5, line 25 with the following rewritten paragraph:

--Figure 4 shows an amino acid sequence ~~encoding KSP-L360~~ for KSP-L360 (amino acids 1-360 of SEQ ID NO: 4) plus the C-terminus myc epitope and 6-histidine tag (collectively SEQ ID NO:4).--

Please replace the paragraph beginning on page 6, line 1 with the following rewritten paragraph:

--Figure 5 shows a nucleic acid sequence encoding a fragment of KSP, termed KSP-K491 herein (nucleotides 1-1473 of SEQ ID NO: 5). KSP-K491 plus the nucleotides encoding a C-terminal myc epitope and a 6-histidine tag collectively include the nucleotides of SEQ ID NO:5. Portions differing from the sequences of Figures 1 and 2 are indicated in bold typeface and are underlined. ~~Residues at the C-terminus include a myc epitope and a 6-histidine tag~~--

Please replace the paragraph beginning on page 6, line 4 with the following rewritten paragraph:

--Figure 6 shows an amino acid sequence ~~encoding for~~ for KSP-K491 (amino acids 1-491 of SEQ ID NO: 6) plus the C-terminus myc epitope and 6-histidine tag (collectively SEQ ID NO:6).--

Please replace the paragraph beginning on page 6, line 5 with the following rewritten paragraph:

--Figure 7 shows a nucleic acid sequence encoding a fragment of KSP, termed KSP-S553 herein (nucleotides 1-1659 of SEQ ID NO: 7). KSP-S553 plus the nucleotides encoding a C-terminal myc epitope and a 6-histidine tag collectively include the nucleotides of SEQ ID NO:7. Portions differing from the sequences of Figures 1 and 2 are indicated in bold typeface and are underlined. ~~Residues at the C-terminus include a myc epitope and a 6-histidine tag~~--

Please replace the paragraph beginning on page 6, line 8 with the following rewritten paragraph:

--Figure 8 shows an amino acid sequence ~~encoding for~~ for KSP-S553 (amino acids 1-553 of SEQ ID NO: 8) plus the C-terminus myc epitope and 6-histidine tag (collectively SEQ ID NO:8).--

Please replace the paragraph beginning on page 6, line 9 with the following rewritten paragraph:

--Figure 9 shows a nucleic acid sequence encoding a fragment of KSP, termed KSP-K368 herein (SEQ ID NO: 9). Portions differing from the sequences of Figures 1 and 2 are indicated in bold typeface and are underlined.--

Please replace the paragraph beginning on page 6, line 12 with the following rewritten paragraph:

--Figure 10 shows an amino acid sequence ~~encoding KSP-S553~~ for KSP-K368 (SEQ ID NO:10).--

Please replace the paragraph beginning on page 6, line 13 with the following rewritten paragraph:

--Figure 11 is a graph showing KSP mRNA levels in matched normal and tumor tissue from breast, lung and colon. ~~MRNA~~ mRNA levels were measured by quantitative PCR relative to a standard. The relative magnitudes of overexpression in each tumor sample relative to the matched normal tissue are displayed above each pair. All values are normalized to the level of KSP mRNA expression observed in cultured HeLa cells.--

Please replace the paragraph beginning on page 4, line 23 with the following replacement paragraph:

--In yet another embodiment herein, a method for inhibiting cellular proliferation is provided which comprises administering to a cell a composition comprising an inhibitor of KSP. In one embodiment, the inhibitor is of human KSP or a fragment thereof. In one embodiment, the inhibitor is specific to human KSP. In one embodiment, KSP inhibitors are any agent which disrupts or inhibits KSP activity as further described herein. In one aspect of the invention, the inhibitor of KSP is a small molecule as further defined herein. Generally, small molecules have a molecular weight of between 50 kD and 2000 kD, and in some cases, less than 1500 kD, or less than 1000kD or less than 500 kD. Examples of KSP inhibitors include but are

not limited to small molecules, ribozymes, antisense molecules and antibodies. KSP inhibitors are further described herein and in ~~the application filed October 27, 1999, entitled Methods and Compositions Utilizing Quinazolinones (serial number not yet received, named inventor Jeffrey T. Finer)~~ U.S. Serial No. 60/198,253, filed October 27, 1999, incorporated by reference in its entirety. The composition which is administered to a cell further comprises an acceptable pharmaceutical carrier in one embodiment. The composition can have a variety of formulations, including, but not limited to those for parental, oral or topical administration.--

Please replace the paragraph beginning on page 9, line 5 and ending on page 9, line 17 with the following:

--Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410 (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266:460-480 (1996); ~~http://blast.wustl.edu/blast/REACRCE.html~~]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).--